

1653



1653

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/870,203A

DATE: 02/05/2002
TIME: 14:00:19

Input Set : A:\4-31452A.ST25.txt
Output Set: N:\CRF3\02052002\I870203A.raw

ENTERED

3 <110> APPLICANT: Novartis AG
 5 <120> TITLE OF INVENTION: Adenovirus particles with mutagenized fiber proteins
 7 <130> FILE REFERENCE: 4-31452A
 9 <140> CURRENT APPLICATION NUMBER: US 09/870,203A
 10 <141> CURRENT FILING DATE: 2001-05-30
 12 <160> NUMBER OF SEQ ID NOS: 43
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1746
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Human adenovirus type 5
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (1)..(1746)
 24 <223> OTHER INFORMATION:
 27 <400> SEQUENCE: 1
 28 atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca 48
 29 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 30 1 5 10 15
 32 tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc 96
 33 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
 34 20 25 30
 36 ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 144
 37 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 38 35 40 45
 40 ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 192
 41 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 42 50 55 60
 44 aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 240
 45 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 46 65 70 75 80
 48 caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 288
 49 Gln Asn Val Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
 50 85 90 95
 52 ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 336
 53 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 54 100 105 110
 56 act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 384
 57 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 58 115 120 125
 60 atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 432
 61 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 62 130 135 140

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64	gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa	480
65	Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln	
66	145 150 155 160	
68	aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act	528
69	Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr	
70	165 170 175	
72	gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg	576
73	Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu	
74	180 185 190	
76	aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg	624
77	Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly	
78	195 200 205	
80	gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act	672
81	Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr	
82	210 215 220	
84	ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act	720
85	Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr	
86	225 230 235 240	
88	gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca	768
89	Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala	
90	245 250 255	
92	gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt	816
93	Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val	
94	260 265 270	
96	agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag	864
97	Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln	
98	275 280 285	
100	gga cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac	912
101	Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn	
102	290 295 300	
104	aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag	960
105	Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu	
106	305 310 315 320	
108	gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata	1008
109	Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile	
110	325 330 335	
112	gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca	1056
113	Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro	
114	340 345 350	
116	aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat	1104
117	Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp	
118	355 360 365	
120	tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac	1152
121	Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp	
122	370 375 380	
124	agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act	1200
125	Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr	
126	385 390 395 400	
128	ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag	1248

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129 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu	415	
130	405	1296
132 aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata		
133 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile		
134	420	1344
136 ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata		
137 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile		
138	435	1392
140 tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat		
141 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn		
142	450	1440
144 gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt		
145 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe		
146 465	470	1488
148 aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga		
149 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly		
150	485	1536
152 ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc		
153 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala		
154	500	1584
156 aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa		
157 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys		
158	515	1632
160 cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac		
161 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp		
162	530	1680
164 aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc		
165 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly		
166 545	550	1728
168 cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca		
169 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser		
170	565	1746
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173 Tyr Ile Ala Gln Glu		
174	580	
177 <210> SEQ ID NO: 2		
178 <211> LENGTH: 581		
179 <212> TYPE: PRT		
180 <213> ORGANISM: Human adenovirus type 5		
182 <400> SEQUENCE: 2		
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188 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro		
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192 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser		
193	35	45
196 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu		
197	50	60
200 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser		

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204	Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn			
205	85	90	95	
208	Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu			
209	100	105	110	
212	Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr			
213	115	120	125	
216	Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile			
217	130	135	140	
220	Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln			
221	145	150	155	160
224	Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr			
225	165.	170	175	
228	Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu			
229	180	185	190	
232	Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly			
233	195	200	205	
236	Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr			
237	210	215	220	
240	Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr			
241	225	230	235	240
244	Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala			
245	245	250	255	
248	Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val			
249	260	265	270	
252	Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln			
253	275	280	285	
256	Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			
257	290	295	300	
260	Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			
261	305	310	315	320
264	Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			
265	325	330	335	
268	Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro			
269	340	345	350	
272	Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp			
273	355	360	365	
276	Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp			
277	370	375	380	
280	Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr			
281	385	390	395	400
284	Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu			
285	405	410	415	
288	Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile			
289	420	425	430	
292	Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile			
293	435	440	445	
296	Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn			
297	450	455	460	

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300 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
301 465 470 475 480
304 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
305 485 490 495
308 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
309 500 505 510
312 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
313 515 520 525
316 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
317 530 535 540
320 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
321 545 550 555 560
324 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
325 565 570 575
328 Tyr Ile Ala Gln Glu
329 580
332 <210> SEQ ID NO: 3
333 <211> LENGTH: 1746
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
338 <223> OTHER INFORMATION: Codes for a mutated Human Adenovirus type 5 fiber protein.
340 <220> FEATURE:
341 <221> NAME/KEY: CDS
342 <222> LOCATION: (1)..(1746)
343 <223> OTHER INFORMATION:
346 <220> FEATURE:
347 <221> NAME/KEY: mutation
348 <222> LOCATION: (1222)..(1227)
349 <223> OTHER INFORMATION:
352 <400> SEQUENCE: 3 48
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355 1 5 10 15
357 tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc 96
358 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
359 20 25 30
361 ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 144
362 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
363 35 40 45
365 ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 192
366 Leu Arg Leu Ser Glu Pro Ieu Val Thr Ser Asn Gly Met Leu Ala Leu
367 50 55 60
369 aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 240
370 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
371 65 70 75 80
373 caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 288
374 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
375 85 90 95

2/5/02

VERIFICATION SUMMARY

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